

WEST Search History

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DATE: Tuesday, August 01, 2006

Hide?	Set Name	Query	Hit Count
		<i>DB=USPT; PLUR=YES; OP=OR</i>	
<input type="checkbox"/>	L17	L16 and (hydroxylase or ketolase or oxygenase)	1
<input type="checkbox"/>	L16	5792903.pn.	1
<input type="checkbox"/>	L15	5792903.pn. and hydroxylase or ketolase or oxygenase	1736
		<i>DB=DWPI; PLUR=YES; OP=OR</i>	
<input type="checkbox"/>	L14	L13 and hydroxylase or ketolase or oxygenase	726
<input type="checkbox"/>	L13	L12 and crt\$	1
<input type="checkbox"/>	L12	WO adj 9628014	2
<input type="checkbox"/>	L11	L10	0
		<i>DB=USPT; PLUR=YES; OP=OR</i>	
<input type="checkbox"/>	L10	(lycopene adj cyclase).clm.	17
		<i>DB=USPT,DWPI; PLUR=YES; OP=OR</i>	
<input type="checkbox"/>	L9	L3 and plant	11
<input type="checkbox"/>	L8	L3 and plant.clm.	2
<input type="checkbox"/>	L7	L3 and marigold	3
		<i>DB=EPAB; PLUR=YES; OP=OR</i>	
<input type="checkbox"/>	L6	CA-2349040-A1.did.	0
		<i>DB=USPT,DWPI; PLUR=YES; OP=OR</i>	
<input type="checkbox"/>	L5	L2	33
<input type="checkbox"/>	L4	L3	11
		<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=OR</i>	
<input type="checkbox"/>	L3	L2 and (crt\$).clm.	35
<input type="checkbox"/>	L2	L1 and (astaxanthin or castaxanthin)	72
<input type="checkbox"/>	L1	crtW and crtZ and crtY	74

END OF SEARCH HISTORY

Sequence Report #3

RESULT 9
 AR022630
 LOCUS AR022630 1650 bp DNA linear PAT 05-DEC-1998
 DEFINITION Sequence 5 from patent US 5792903.
 ACCESSION AR022630
 VERSION AR022630.1 GI:3976692
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 1650)
 AUTHORS Hirschberg, J., Cunningham, F. Xavier. Jr. and Gantt, E.
 TITLE Lycopene cyclase gene
 JOURNAL Patent: US 5792903-A 5 11-AUG-1998;
 FEATURES Location/Qualifiers
 source 1. .1650
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.:	3.77e-261	Length:	1650
Score:	2622.00	Matches:	499
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	99.8%	Mismatches:	0
Query Match:	99.8%	Indels:	0
DB:	2	Gaps:	0

US-10-524-827-18 (1-500) x AR022630 (1-1650)

Qy	1	MetAspThrLeuLeuLysThrProAsnAsnLeuGluPheLeuAsnProHisHisGlyPhe	20
Db	112	ATGGATACTTTGTTGAAAACCCAAATAACCTTGAATTTCTGAACCCACATCATGGTTTT	171
Qy	21	AlaValLysAlaSerThrPheArgSerGluLysHisHisAsnPheGlySerArgLysPhe	40
Db	172	GCTGTAAAGCTAGTACCTTTAGATCTGAGAAGCATCATAATTTGGTTCTAGGAAGTTT	231
Qy	41	CysGluThrLeuGlyArgSerValCysValLysGlySerSerSerAlaLeuLeuGluLeu	60
Db	232	TGTGAAACTTTGGGTAGAAGTGTGTGTTAAGGGTAGTAGTAGTGCTCTTTTAGAGCTT	291
Qy	61	ValProGluThrLysLysGluAsnLeuAspPheGluLeuProMetTyrAspProSerLys	80
Db	292	GTACCTGAGACCAAAAAGGAGAATCTTGATTTTGAGCTTCCTATCTATGACCCTTCAAAA	351
Qy	81	GlyValValValAspLeuAlaValValGlyGlyGlyProAlaGlyLeuAlaValAlaGln	100
Db	352	GGGGTTGTTGTGGATCTTGCTGTGGTTGGTGGGCCCTGCAGGACTTGCTGTTGCACAG	411
Qy	101	GlnValSerGluAlaGlyLeuSerValCysSerIleAspProAsnProLysLeuIleTrp	120
Db	412	CAAGTTTCTGAAGCAGGACTCTCTGTTTGTTCGAATTGATCCGAATCCTAAATTGATATGG	471
Qy	121	ProAsnAsnTyrGlyValTrpValAspGluPheGluAlaMetAspLeuLeuAspCysLeu	140
Db	472	CCTAATAACTATGGTGTGTTGGGTGGATGAATTTGAGGCTATGGACTTGTTAGATTGTCTA	531
Qy	141	AspAlaThrTrpSerGlyAlaAlaValTyrIleAspAspAsnThrAlaLysAspLeuHis	160
Db	532	GATGCTACCTGGTCTGGTGAGCAGTGACATTGATGATAATACGGCTAAAGATCTTCAT	591

Qy	161	ArgProTyrGlyArgValAsnArgLysGlnLeuLysSerLysMetMetGlnLysCysIle	180
Db	592	AGACCTTATGGAAGGGTTAACCGGAAACAGCTGAAATCGAAAATGATGCAGAAATGTATA	651
Qy	181	MetAsnGlyValLysPheHisGlnAlaLysValIleLysValIleHisGluGluSerLys	200
Db	652	ATGAATGGTGTAAATTCCACCAAGCCAAAGTTATAAAGGTGATTCATGAGGAATCGAAA	711
Qy	201	SerMetLeuIleCysAsnAspGlyIleThrIleGlnAlaThrValValLeuAspAlaThr	220
Db	712	TCCATGTTGATATGCAATGATGGTATTACTATTCAGGCAACGGTGGTGCTCGATGCAACT	771
Qy	221	GlyPheSerArgSerLeuValGlnTyrAspLysProTyrAsnProGlyTyrGlnValAla	240
Db	772	GGCTTCTCTAGATCTCTTGTTCAAGTATGATAAGCCTTATAACCCCGGTATCAAGTTGCT	831
Qy	241	TyrGlyIleLeuAlaGluValGluGluHisProPheAspValAsnLysMetValPheMet	260
Db	832	TATGGCATTTTGGCTGAAGTGAAGAGCACCCCTTGATGTAAACAAGATGGTTTTCATG	891
Qy	261	AspTrpArgAspSerHisLeuLysAsnAsnThrAspLeuLysGluArgAsnSerArgIle	280
Db	892	GATTGGCGAGATTCTCATTTGAAGACAATACTGATCTCAAGGAGAGAAATAGTAGAATA	951
Qy	281	ProThrPheLeuTyrAlaMetProPheSerSerAsnArgIlePheLeuGluGluThrSer	300
Db	952	CCAACTTTTCTTTATGCAATGCCATTTTCATCCAACAGGATATTTCTTGAAGAAACATCA	1011
Qy	301	LeuValAlaArgProGlyLeuArgIleAspAspIleGlnGluArgMetValAlaArgLeu	320
Db	1012	CTCGTAGCTCGTCCTGGCTTGGTATAGATGATATTCAAGAACGAATGGTGGCTCGTTTA	1071
Qy	321	AsnHisLeuGlyIleLysValLysSerIleGluGluAspGluHisCysLeuIleProMet	340
Db	1072	AACCATTGTTGGGATAAAAGTGAAGAGCATTGAAGAAGATGAACATTGTCTAATACCAATG	1131
Qy	341	GlyGlyProLeuProValLeuProGlnArgValValGlyIleGlyGlyThrAlaGlyMet	360
Db	1132	GGTGGTCCACTCCAGTATTACCTCAGAGAGTCGTTGGAATCGGTGGTACAGCTGGCATG	1191
Qy	361	ValHisProSerThrGlyTyrMetValAlaArgThrLeuAlaAlaAlaProValValAla	380
Db	1192	GTTTCATCCATCCACCGGTTATATGGTGGCAAGGACACTAGCTGCGGCTCCTGTTGTGCC	1251
Qy	381	AsnAlaIleIleGlnTyrLeuGlySerGluArgSerHisSerGlyAsnGluLeuSerThr	400
Db	1252	AATGCCATAATTCAATACCTCGGTTCTGAAAGAAGTCATTGCGGTAATGAATTATCCACA	1311
Qy	401	AlaValTrpLysAspLeuTrpProIleGluArgArgArgGlnArgGluPhePheCysPhe	420
Db	1312	GCTGTTTGGAAAGATTTGTGGCCTATAGAGAGGAGACGTCAAAGAGAGTTCTTCTGCTTC	1371
Qy	421	GlyMetAspIleLeuLeuLysLeuAspLeuProAlaThrArgArgPhePheAspAlaPhe	440
Db	1372	GGTATGGATATTCTTCTGAAGCTTGATTACCTGCTACAAGAAGGTTCTTTGATGCATTC	1431
Qy	441	PheAspLeuGluProArgTyrTrpHisGlyPheLeuSerSerArgLeuPheLeuProGlu	460
Db	1432	TTTGACTTAGAACCTCGTTATTGGCATGGCTTCTATCGTCTCGATTGTTTCTACCTGAA	1491

Qy	461	LeuIleValPheGlyLeuSerLeuPheSerHisAlaSerAsnThrSerArgPheGluIle	480
Db	1492	CTCATAGTTTTTGGGCTGTCTCTATTCTCTCATGCTTCAAATACTTCTAGATTGAGATA	1551
Qy	481	MetThrLysGlyThrValProLeuValAsnMetIleAsnAsnLeuLeuGlnAspLysGlu	500
Db	1552	ATGACAAAGGGAAGTTCATTAGTAAATATGATCAACAATTTGTTACAGGATAAAGAA	1611

Sequence Report #2

RESULT 1

AAC65654

ID AAC65654 standard; DNA; 1608 BP.

XX

AC AAC65654;

XX

DT 16-FEB-2001 (first entry)

XX

DE H. pluvialis carotene hydroxylase DNA.

XX

KW Carotene hydroxylase; beta-carotene; zeaxanthine; canthaxanthine;
 KW astaxanthine; biocatalyst; xanthophyll; beta-ionone; 4-keto-beta-ionone;
 KW 3-hydroxy-beta-ionone; 3-hydroxy-4-keto-beta-ionone; plant; nutrition;
 KW colorant; vitamin A precursor; immunostimulant; cancer-prevention;
 KW antioxidant; ds.

XX

OS Haematococcus pluvialis.

XX

FH Key Location/Qualifiers

FT CDS

1. .971

FT /*tag= a

FT /product= "carotene hydroxylase"

FT /note= "no start codon given"

XX

PN DE19916140-A1.

XX

PD 12-OCT-2000.

XX

PF 09-APR-1999; 99DE-01016140.

XX

PR 09-APR-1999; 99DE-01016140.

XX

PA (BADI) BASF AG.

XX

PI Linden H, Sandmann G;

XX

DR WPI; 2000-657331/64.

XX

DR P-PSDB; AAB11111.

XX

PT New recombinant algal carotene hydroxylase protein useful for converting
 PT carotenes to xanthophylls, e.g. for use in human and animal nutrition.

XX

PS Claim 4; Page 12-14; 18pp; German.

XX

CC This invention describes a novel recombinant Haematococcus pluvialis
 CC carotene hydroxylase protein (I) which is capable of converting beta-
 CC carotene to zeaxanthine and/or converting canthaxanthine to astaxanthine.
 CC (I) is useful as a biocatalyst for producing xanthophylls by converting a
 CC beta-ionone structural element into a 3-hydroxy-beta-ionone structural
 CC element and/or converting a 4-keto-beta-ionone structural element into a
 CC 3-hydroxy-4-keto-beta-ionone structural element. Nucleic acids encoding
 CC (I) are useful for producing genetically modified organisms, especially
 CC plants, exhibiting increased expression of xanthophylls. Xanthophylls are
 CC important in human and animal nutrition as colorants and vitamin A
 CC precursors, have health-promoting (e.g. immunostimulant) properties, and
 CC have cancer-preventing antioxidant activity

XX

SQ Sequence 1608 BP; 327 A; 414 C; 513 G; 354 T; 0 U; 0 Other;

Query Match 100.0%; Score 1608; DB 3; Length 1608;

Best Local Similarity 100.0%; Pred. No. 0;

		Matches 1608; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	CTACATTTTACAAGCCCGTGAGCGGTGCAAGCGCTCTGCCCCACATCGGCCACCTCCTC	60
Db	1	CTACATTTTACAAGCCCGTGAGCGGTGCAAGCGCTCTGCCCCACATCGGCCACCTCCTC	60
Qy	61	ATCTCCATCGGTCATTTGCTGCTACCACGATGCTGTGGAAGCTGCAGTCAATCAGCGTCA	120
Db	61	ATCTCCATCGGTCATTTGCTGCTACCACGATGCTGTGGAAGCTGCAGTCAATCAGCGTCA	120
Qy	121	AGGCCCGCCGCGTTGAACTAGCCCGCGACATCACGCGGCCCAAAGTCTGCCTGCATGCTC	180
Db	121	AGGCCCGCCGCGTTGAACTAGCCCGCGACATCACGCGGCCCAAAGTCTGCCTGCATGCTC	180
Qy	181	AGCGGTGCTCGTTAGTTGCGCTGCGAGTGGCAGCACACAGACAGAGGAGGCGCTGGGAA	240
Db	181	AGCGGTGCTCGTTAGTTGCGCTGCGAGTGGCAGCACACAGACAGAGGAGGCGCTGGGAA	240
Qy	241	CCGTGCAGGCTGCCGGCGCGGGCGATGAGCACAGCGCCGATGTAGCACTCCAGCAGCTTG	300
Db	241	CCGTGCAGGCTGCCGGCGCGGGCGATGAGCACAGCGCCGATGTAGCACTCCAGCAGCTTG	300
Qy	301	ACCGGGCTATCGCAGAGCGTCGTGCCCGGCGCAAACGGGAGCAGCTGTCATACCAGGCTG	360
Db	301	ACCGGGCTATCGCAGAGCGTCGTGCCCGGCGCAAACGGGAGCAGCTGTCATACCAGGCTG	360
Qy	361	CCGCCATTGCAGCATCAATTGGCGTGTGAGGCATTGCCATCTTCGCCACCTACCTGAGAT	420
Db	361	CCGCCATTGCAGCATCAATTGGCGTGTGAGGCATTGCCATCTTCGCCACCTACCTGAGAT	420
Qy	421	TTGCCATGCACATGACCGTGGGCGGCGCAGTGCCATGGGGTGAAGTGGCTGGCACTCTCC	480
Db	421	TTGCCATGCACATGACCGTGGGCGGCGCAGTGCCATGGGGTGAAGTGGCTGGCACTCTCC	480
Qy	481	TCTTGGTGGTTGGTGGCGCGCTCGGCATGGAGATGTATGCCCGCTATGCACACAAAGCCA	540
Db	481	TCTTGGTGGTTGGTGGCGCGCTCGGCATGGAGATGTATGCCCGCTATGCACACAAAGCCA	540
Qy	541	TCTGGCATGAGTCGCCTCTGGGCTGGCTGCTGCACAAGAGCCACCACACACCTCGCACTG	600
Db	541	TCTGGCATGAGTCGCCTCTGGGCTGGCTGCTGCACAAGAGCCACCACACACCTCGCACTG	600
Qy	601	GACCCTTTGAAGCCAACGACTTGTTTGAATCATCAATGGACTGCCCGCCATGCTCCTGT	660
Db	601	GACCCTTTGAAGCCAACGACTTGTTTGAATCATCAATGGACTGCCCGCCATGCTCCTGT	660
Qy	661	GTACCTTTGGCTTCTGGCTGCCCAACGTCTGGGGGCGGCCTGCTTTGGAGCGGGGCTGG	720
Db	661	GTACCTTTGGCTTCTGGCTGCCCAACGTCTGGGGGCGGCCTGCTTTGGAGCGGGGCTGG	720
Qy	721	GCATCAGCTATACGGCATGGCATATATGTTTGTACACGATGGCCTGGTGACAGGCGCT	780
Db	721	GCATCAGCTATACGGCATGGCATATATGTTTGTACACGATGGCCTGGTGACAGGCGCT	780
Qy	781	TTCCACCGGGGCCATCGCTGGCCTGCCCTACATGAAGCGCCTGACAGTGGCCCAACAGC	840
Db	781	TTCCACCGGGGCCATCGCTGGCCTGCCCTACATGAAGCGCCTGACAGTGGCCCAACAGC	840
Qy	841	TACACCACAGCGGCAAGTACGGTGGCGCGCCCTGGGGTATGTTCTTGGGTCCACAGGAGC	900
Db	841	TACACCACAGCGGCAAGTACGGTGGCGCGCCCTGGGGTATGTTCTTGGGTCCACAGGAGC	900

Qy	901	TGCAGCACATTCCAGGTGCGGCGGAGGAGGTGGAGCGACTGGTCCTGGAACGGACTGGT	960
Db	901	TGCAGCACATTCCAGGTGCGGCGGAGGAGGTGGAGCGACTGGTCCTGGAACGGACTGGT	960
Qy	961	CCAAGCGGTAGGGTGCGGAACCAGGCACGCTGGTTTCACACCTCATGCCTGTGATAAGGT	1020
Db	961	CCAAGCGGTAGGGTGCGGAACCAGGCACGCTGGTTTCACACCTCATGCCTGTGATAAGGT	1020
Qy	1021	GTGGCTAGAGCGATGCGTGTGAGACGGGTATGTCACGGTCGACTGGTCTGATGGCCAATG	1080
Db	1021	GTGGCTAGAGCGATGCGTGTGAGACGGGTATGTCACGGTCGACTGGTCTGATGGCCAATG	1080
Qy	1081	GCATCGGCCATGTCTGGTCATCACGGGCTGGTTGCCTGGGTGAAGGTGATGCACATCATC	1140
Db	1081	GCATCGGCCATGTCTGGTCATCACGGGCTGGTTGCCTGGGTGAAGGTGATGCACATCATC	1140
Qy	1141	ATGTGCGGTTGGAGGGGCTGGCACAGTGTGGGCTGAACTGGAGCAGTTGTCCAGGCTGGC	1200
Db	1141	ATGTGCGGTTGGAGGGGCTGGCACAGTGTGGGCTGAACTGGAGCAGTTGTCCAGGCTGGC	1200
Qy	1201	GTTGAATCAGTGAGGGTTTGTGATTGGCGGTTGTGAAGCAATGACTCCGCCCATTCTTA	1260
Db	1201	GTTGAATCAGTGAGGGTTTGTGATTGGCGGTTGTGAAGCAATGACTCCGCCCATTCTTA	1260
Qy	1261	TTTGTGGGAGCTGAGATGATGGCATGCTTGGGATGTGCATGGATCATGGTAGTGACAGAA	1320
Db	1261	TTTGTGGGAGCTGAGATGATGGCATGCTTGGGATGTGCATGGATCATGGTAGTGACAGAA	1320
Qy	1321	ACTATATTCACCTAGGGCTGTTGGTAGGATCAGGTGAGGCCTTGACATTGCATGATGTA	1380
Db	1321	ACTATATTCACCTAGGGCTGTTGGTAGGATCAGGTGAGGCCTTGACATTGCATGATGTA	1380
Qy	1381	CTCGTCATGGTGTGTTGGTGAGAGGATGGATGTGGATGGATGTGTATTCTCAGACGTAGA	1440
Db	1381	CTCGTCATGGTGTGTTGGTGAGAGGATGGATGTGGATGGATGTGTATTCTCAGACGTAGA	1440
Qy	1441	CCTTGACTGGAGGCTTGATCGAGAGAGTGGGCCGTATTCTTTGAGAGGGGAGGCTCGTGC	1500
Db	1441	CCTTGACTGGAGGCTTGATCGAGAGAGTGGGCCGTATTCTTTGAGAGGGGAGGCTCGTGC	1500
Qy	1501	CAGAAATGGTGAGTGGATGACTGTGACGCTGTACATTGCAGGCAGGTGAGATGCACTGTC	1560
Db	1501	CAGAAATGGTGAGTGGATGACTGTGACGCTGTACATTGCAGGCAGGTGAGATGCACTGTC	1560
Qy	1561	TCGATTGTAAATACATTTCAGATGCAAAAAAAAAAAAAAAAAAAAAA	1608
Db	1561	TCGATTGTAAATACATTTCAGATGCAAAAAAAAAAAAAAAAAAAAAA	1608

Sequence Report #1

RESULT 1

AF2204

beta-carotene ketolase [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C;Accession: AF2204

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguc

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AF2204

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-258

A;Cross-references: UNIPROT:Q8YSA0; UNIPARC:UPI000000CE6D5; GB:BA000019; PIDN:BAB74888.

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: alr3189

C;Superfamily: beta-carotene ketolase

Query Match 100.0%; Score 1439; DB 2; Length 258;
 Best Local Similarity 100.0%; Pred. No. 2.9e-116;
 Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MVQCQPSSLHSEKLVLLSSTIRDDKNINKGIFIACFILFLWAISLILLLSIDTSIIHKSL 60
          |||
Db      1 MVQCQPSSLHSEKLVLLSSTIRDDKNINKGIFIACFILFLWAISLILLLSIDTSIIHKSL 60

Qy     61 LGIAMLWQTFLYTGLFITAH DAMHGVVYPKNPRINNF I GKLTLILYGLLPYKD L LK KHWL 120
          |||
Db     61 LGIAMLWQTFLYTGLFITAH DAMHGVVYPKNPRINNF I GKLTLILYGLLPYKD L LK KHWL 120

Qy    121 HHGHPGTDLD PDY YNGHPQNFFLWYLHFMKSYWRWTQIFGLVMI FHGLKNLVH I PENNLI 180
          |||
Db    121 HHGHPGTDLD PDY YNGHPQNFFLWYLHFMKSYWRWTQIFGLVMI FHGLKNLVH I PENNLI 180

Qy    181 IFWMIP SILSSVQLFYFGTFLPHKKLEGGYTNP HCARS I PLPLFWSFVTCYHFGYHKEHH 240
          |||
Db    181 IFWMIP SILSSVQLFYFGTFLPHKKLEGGYTNP HCARS I PLPLFWSFVTCYHFGYHKEHH 240

Qy    241 EYPQLPWWKLPEAHKISL 258
          |||
Db    241 EYPQLPWWKLPEAHKISL 258

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RESULT 2